Scope and Access

Clone DB is an Entrez database from NCBI that replaces and expands upon the former Clone Registry to represent a broader range of eukaryotic organisms and clone types. Clone DB integrates information about clones and their source libraries, including sequence data, genome map positions and distributor information. This consolidation provides a more comprehensive view of clone-associated data and makes clone selections for various experimental purposes a straightforward process. Clone DB has records for genomic and cell-based (gene-trap and gene-targeting) libraries and clones representing more than 100 different eukaryotic taxa.

Resources ☑ How To ☑

Sign in to NCBI

Filter by Creator

Contact: info@ncbi.nlm.nih.gov

Several venues are available for accessing data from CloneDB: Text searching via the Clone DB homepage

S NCBI

Bulk download from the clone FTP site

Locating clones via CloneFinder

https://www.ncbi.nlm.nih.gov/clone/ ftp://ftp.ncbi.nih.gov/repository/clone/

https://www.ncbi.nlm.nih.gov/mapview/mvhome/clonehome.html

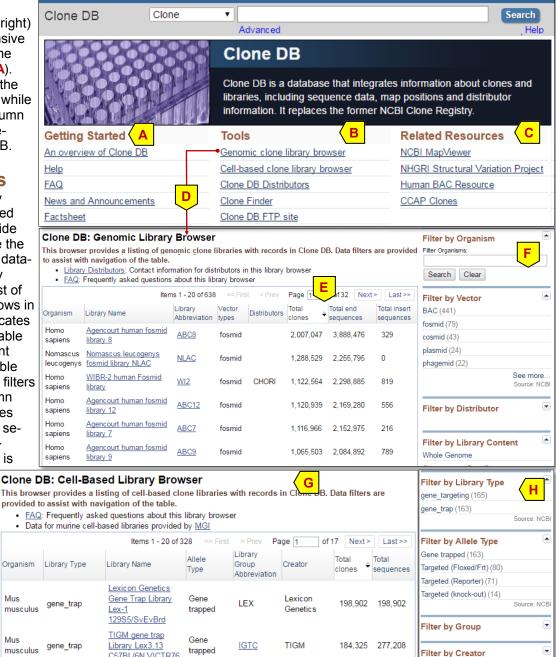
The Homepage

The Clone DB homepage (right) provide links to comprehensive online help documents in the "Getting Started" column (A). The Tools column (B) lists the tools specific to Clone DB, while the Related Resources column (C) lists representative resources related to Clone DB.

Browsing Records

The "Genomic clone library browser" and the "Cell-based clone library browser" provide convenient ways to browse the libraries available from the database. The Genomic Library Browser (D) displays the list of libraries in a table. The arrows in the column header (E) indicates the attribute by which the table is sorted. Clicking a different column header sorts the table by that attribute. Additional filters (F) in the right-hand column allows you to restrict libraries displayed to those with the selected properties. The Cell-Based Library Browser (G) is similar to that of the Ge-

nomic Library Browser. The library attributes (column headers) and the filters (H, shown in part) are specific to the library types. The search examples shown in subsequent pages are from genomic clone data. Similar library and clone records also exist for cellbased clones.



trapped

C57BL/6N VICTR76

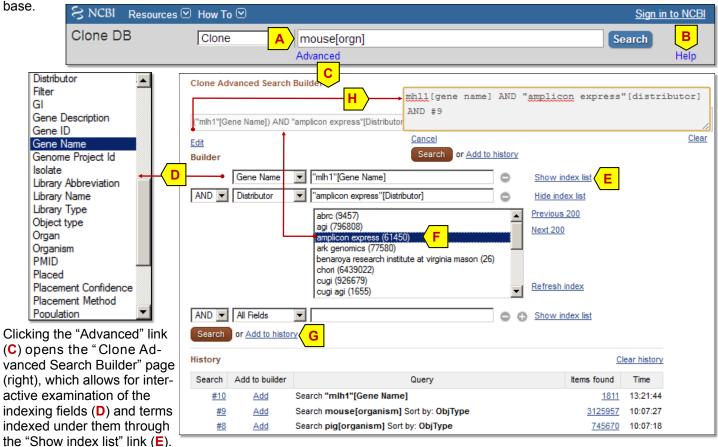
Organism

Mus

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Searching for Clones

Searching for clones with custom text can be done using the query box and the Search button (A) at the top of the Clone DB homepage. Clinking the "Help" link (B) opens an online document, providing more details on how to use this database.



Selected query terms are automatically entered in the query box (F). Clicking the "Add to history" link (G) previews the search result by adding an entry in the "History" section. Clicking the "Edit" link (H) unlocks the query box so custom terms such as a search history (#9) can be added.

Displaying the Search Results

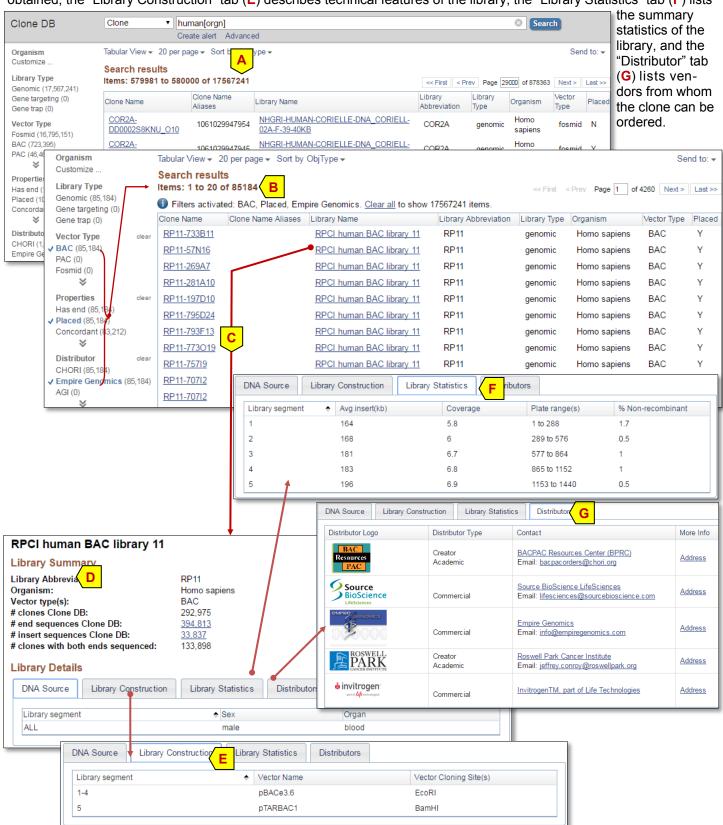
A search result is displayed in "Tabular View" (below), which lists the clone name, the source library, library type, vector type, and mapping status (H). The display format, number of records displayed, and sorting order can be customized using pull-down menus (I) at the top. Filters (J) in the left-hand column of a search result can quickly narrow down the



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Detailed Library Record View

Searching with "human[orgn]" retrieve a long list of clones (A). Using filters in the left hand column, the list can be reduced to a specific subset of interest. The example (B) is from filtering for bac clone with genome placement, from a selected provider (Empire Genomics). Clicking a library name in the "Library name" column opens a detailed display for that library (C), which provides a summary of the displayed library as well as other technical details in tabular format under different tabs. For example, the "DNA Source" tab (D) provides details about the organism from which the DNA was obtained, the "Library Construction" tab (E) describes technical features of the library, the "Library Statistics" tab (F) lists



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Clone

Detailed Genomic Clone Record View

Clone DB

A clone's utility as a research reagent is greatly improved when its genomic location is known. Clone DB maps genomic clones to Ref-Seg assemblies annotated via the NCBI annotation pipeline. This subset of clones can be retrieved using a field-limited term of "placed" [prop] as shown in the search example (A), which also uses a gene symbol to further narrow the scope of the search.

Clicking the clone name (B) opens the individual clone record, which provides a summary of important features along with an ideogram showing the clone's genomic location (C).

The "Genome View" tab (D) graphically displays the genomic annotation of the region, to which the clone is mapped. The clone mapping details are given below (E), with the specific clone highlighted. Hovering over a clone opens a popup (F) to provide additional technical details. This interactive display is based on the Graphical Sequence Viewer [1,2].

Other tabs provide additional details: the "Clone Placements" tab (G) lists clone mapping in text format, the "Associated Sequences" tab (H) lists relevant GenBank entries for the clone, and the "Distributors" tab (1) lists the vendors for this clone with the vendors' contact information given in the linked page.

Sequence-Based Placements ③

Primary Assembly 13

Seg ID

Email: dnabank@brc.riken.jp

13

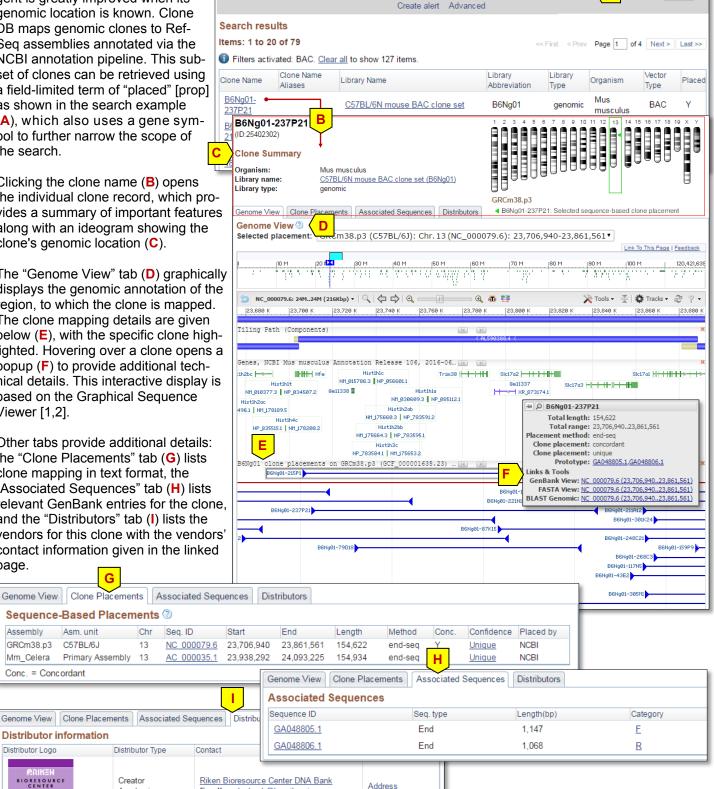
Distributor Type

Creator

Academic

Asm unit

C57BL/6J



▼ mouse[orgn] AND placed[prop] AND hfe[gene]

0 Search

References

Assembly

GRCm38.p3

Distributor Logo

Conc. = Concordant

Distributor information

- 1. Sequence Viewer online Help
- 2. Sequence Viewer factsheet

https://www.ncbi.nlm.nih.gov/tools/sviewer/ https://ftp.ncbi.nlm.nih.gov/pub/factsheets/Factsheet Graphical SV.pdf